

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Mack, David H.

(ii) TITLE OF INVENTION: COMPUTER-AIDED VISUALIZATION OF EXPRESSION COMPARISON

iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Joe Liebeschuetz of Townsend and Townsend and Crew LLP
(B) STREET: Two Embarcadero Center, Eighth Floor
(C) CITY: San Francisco
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94111-3834

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/020,743
(B) FILING DATE: 09-FEB-1998
(C) CLASSIFICATION:

viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Liebeschuetz, Joe
(B) REGISTRATION NUMBER: 37,505
(C) REFERENCE/DOCKET NUMBER: 018547034800US

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (650) 326-2400
(B) TELEFAX: (650) 326-2422

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2691 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGAGACAGAC AGACAGCTGG CAAGAGGCAG CCTGGGGGCC ACAGCTGCTT CAGCAGACCT	60
CATGGCTGAG TGAGCCTCCC CTGGGCCAG CACCCCACCT CAGCATGGTC CAAGCCCATG	120
GGGGCGCTC CAGAGCACAG CCGTTGACCT TGTCTTGAG GGCAGCCATG ACCCAGCCTC	180
CGCCTGAAAA AACGCCAGCC AAGAAGCATG TGCGACTGCA GGAGAGGCCGG GGCTCCAATG	240
TGGCTCTGAT GCTGGACGTT CGGTCCCTGG GGGCCGTAGA ACCCATCTGC TCTGTGAACA	300
CACCCCGGGA GGTCACCCCTA CACTTCTGC GCACTGCTGG ACACCCCCCTT ACCCGCTGGG	360
CCCTTCAGCG CCAGCCACCC AGCCCCAAGC AACTGGAAGA AGAATTCTTG AAGATCCCTT	420
CAAACTTTGT CAGCCCCGAA GACCTGGACA TCCCTGGCCA CGCCTCCAAG GACCGATACA	480
AGACCATCTT GCCAAATCCC CAGAGCCGTG TCTGTCTAGG CCGGGCACAG AGCCAGGAGG	540
ACGGAGATTA CATCAATGCC AACTACATCC GAGGCTATGA CGGGAAAGGAG AAGGTCTACA	600
TTGCCACCCA GGGCCCCATG CCCAACACTG TGTGGACTT CTGGGAGATG GTGTGGCAAG	660
AGGAAGTGTGTC CCTCATTGTC ATGCTCACTC AGCTCCGAGA GGGCAAGGAG AAATGTGTCC	720
ACTACTGGCC CACAGAAGAG GAAACCTATG GACCCTTCCA GATCCGCATC CAGGACATGA	780
AAGAGTGCCTC AGAATACACT GTGCGGCAGC TCACCATCCA GTACCAGGAA GAGCGCCGGT	840
CAGTAAAGCA CATCCCTTT TCAGGCTGGC CAGACCATCA GACACCAGAA TCAGCTGGC	900
CCCTGCTGCG CCTAGTGGCA GAGGTGGAGG AGAGCCCCGA GACAGCCGCC CACCCGGGC	960
CTATCGTAGT CCACTGCAGT GCAGGGATTG GCCGGACGGG CTGCTTCATC GCCACGCGAA	1020
TTGGCTGTCA ACAGCTGAAA GCCCGAGGAG AAGTGGACAT TCTGGGTATT GTGTGCCAAC	1080
TGCGGCTAGA CAGAGGGGGG ATGATCCAGA CGGACGAGCA GTACCAGTTT CTGCACCACA	1140
CTTTGGCCCT GTATGCAGGC CAGCTGCCTG AGGAACCCAG CCCCTGACCC CTGCCACCC	1200
CCGGTGGCCC AGGTGCCTAC CTCCCTCAAG CCTGGGAAGT CACAGGAAGC AGCAGCAGTA	1260
AGGACAAGGG GCCGGATTCC AGGTCTCAA CACTGGCAC TCCTCTGCTT CCTCTGTTGG	1320
CCCCAGATGG ACAGTAAGGG GAACCTCCAA TGTCTCTCTG AACTTAAAGA CAGGAGCTGG	1380
CATTTATGAC AGACAAAGAA AGAAGCCAG GTGTCTGGT GTTCTCTGAG ACACCTTTG	1440
TGAGCTTCAG TTTCCTGTT TATAACATGA ACATAAGTGC TTAGCTGCCA TGAGGGAAAA	1500
GTAATGAGAG AAGTTCTAG AAGCCACTCC AGCCACTCCT TCCTGGGCT GACAAAAGGG	1560
TGATTCCAAG ATCATCCTTC ACCCGAGGTC CTGCCAAGC ACAGGCCAGA TGCAAGAATG	1620
GGGAAAAGTC TGGTCTGAT CTCCAAGTCT CAACATCCTA TCAGTGACTC TGCTCCCTGA	1680

CCACACATCG	GAAGGGCTGG	ATGACCCCAA	TCAAAAGAAA	GAACAAGGAC	TCTGGTTACC	1740
CTTGCCTCC	ACCCATGTGT	CATAAGAGTA	GGCTACAGAG	GTGACCAGGC	CTGGCAGTTG	1800
AAATCTCTGG	AAGAGGGAAC	ATGTGGGGAC	TACTCAGAGG	CAAAGAGGAG	CTGCTCCTGC	1860
CTCCATGGTT	GCTGGCCACT	CCCACCAACT	ACTCTTAGGG	AGGCTAAGCA	GTCTCTGTTT	1920
TGCTTCCATG	GCTCAAATAA	TACCCCTGGGT	ATGCAGGACC	CACTATACCT	TGCATTTGCT	1980
GGTACACCTA	GAGAGCTTGG	CTGTTCCAA	AAACAATCAG	GGTCATAACC	ATCCATGCAG	2040
ACATGGAGGC	TCGGCTGAAC	CAGGACTCCT	CACTGTCTAC	CTGAGAGAAT	GAGCACCCCT	2100
CATCCATCTC	AGCATCAACA	CAATTCCAG	GGGACCTCAG	GTCTACCTCA	GGACTGAACG	2160
CCACACCTCA	GGATTCCCTCC	TCCTTGAATC	TGAGACTGGC	TGCCCATATTCT	GAGATGGGGA	2220
TGAAGGTAAG	ATGCCGCATC	ACCAGGCACG	CCGCCCCCTGA	CAGCTGCCTT	GATAACCAGCT	2280
CTCTGTGGAA	ACCCCCGAGG	AGTTGGATCT	GGAGAACAGC	TGGGCCTCCT	CACTCAGGAC	2340
TTCTCTCCTG	AAGAACACGC	AGTGCTAAAA	CTGAGGATGA	TTTCCCTAAT	GCTTCTGCTT	2400
GGCCTTATGG	AGGAGCTGCT	CCTTCCTTAC	AGCCTTGGGG	ATGGACTTGC	CCACACCTCC	2460
ACCTCCCCCTG	AGCCCTGTGA	GAGGCACGAC	TGTCTATGCC	AATGAGGCTC	GGTGGGGGGC	2520
TCTCAAGTGC	CTGATCCTGC	CCTGGGCTCA	GAGCCAGCCC	AGAGGGAAGC	AACTGCACAG	2580
CCCCACAGGC	CCTCCCTGGC	ACTGTCCCCC	CAACCCCCATC	TCAGAGCTCA	GAGGGTACAA	2640
GCTCCAGAAC	AGTAACCAAG	TGGGAAAATA	AAGACTTCTT	GGATGACTGA	C	2691

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relev

(二二) 附录二

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Val Gln Ala His Gly Gly Arg Ser Arg Ala Gln Pro Leu Thr Leu
 1 5 10 15

Ser Leu Gly Ala Ala Met Thr Gln Pro Pro Pro Glu Lys Thr Pro Ala
 20 25 30

Lys Lys His Val Arg Leu Gln Glu Arg Arg Gly Ser Asn Val Ala Leu
 35 40 45

Met Leu Asp Val Arg Ser Leu Gly Ala Val Glu Pro Ile Cys Ser Val
 50 55 60

Asn Thr Pro Arg Glu Val Thr Leu His Phe Leu Arg Thr Ala Gly His
 65 70 75 80

Pro Leu Thr Arg Trp Ala Leu Gln Arg Gln Pro Pro Ser Pro Lys Gln
 85 90 95

Leu Glu Glu Glu Phe Leu Lys Ile Pro Ser Asn Phe Val Ser Pro Glu
 100 105 110

Asp Leu Asp Ile Pro Gly His Ala Ser Lys Asp Arg Tyr Lys Thr Ile
 115 120 125

Leu Pro Asn Pro Gln Ser Arg Val Cys Leu Gly Arg Ala Gln Ser Gln
 130 135 140

Glu Asp Gly Asp Tyr Ile Asn Ala Asn Tyr Ile Arg Gly Tyr Asp Gly
 145 150 155 160

Lys Glu Lys Val Tyr Ile Ala Thr Gln Gly Pro Met Pro Asn Thr Val
 165 170 175

Ser Asp Phe Trp Glu Met Val Trp Gln Glu Glu Val Ser Leu Ile Val
 180 185 190

Met Leu Thr Gln Leu Arg Glu Gly Lys Glu Lys Cys Val His Tyr Trp
 195 200 205

Pro Thr Glu Glu Glu Thr Tyr Gly Pro Phe Gln Ile Arg Ile Gln Asp
 210 215 220

Met Lys Glu Cys Pro Glu Tyr Thr Val Arg Gln Leu Thr Ile Gln Tyr
 225 230 235 240

Gln Glu Glu Arg Arg Ser Val Lys His Ile Leu Phe Ser Ala Trp Pro
 245 250 255

Asp His Gln Thr Pro Glu Ser Ala Gly Pro Leu Leu Arg Leu Val Ala
 260 265 270

Glu Val Glu Glu Ser Pro Glu Thr Ala Ala His Pro Gly Pro Ile Val
 275 280 285

Val His Cys Ser Ala Gly Ile Gly Arg Thr Gly Cys Phe Ile Ala Thr
290 295 300

Arg Ile Gly Cys Gln Gln Leu Lys Ala Arg Gly Glu Val Asp Ile Leu
305 310 315 320

Gly Ile Val Cys Gln Leu Arg Leu Asp Arg Gly Gly Met Ile Gln Thr
325 330 335

Asp Glu Gln Tyr Gln Phe Leu His His Thr Leu Ala Leu Tyr Ala Gly
340 345 350

Gln Leu Pro Glu Glu Pro Ser Pro
355 360

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